#12 |652

1600

P.6

RAW SEQUENCE LISTING   DATE: 11/13/2002
PATENT APPLICATION: US/09/701,586C   TIME: 15:44:32

Input Set : A:\701586sq
Output Set: N:\CRF4\11132002\I701586C.raw

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  3 <110> APPLICANT: Kock, Michael
  4         Hoeger, Thomas
  5         Kroeger, Burkhard
  6         Otterbach, Bernd
  7         Lubisch, Wilfried
  8         Lemaire, Hans-Georg
 10 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene
 12 <130> FILE REFERENCE: 0050/49100
 14 <140> CURRENT APPLICATION NUMBER: US 09/701,586C
C--> 15 <141> CURRENT FILING DATE: 2000-11-30
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889
 18 <151> PRIOR FILING DATE: 1999-06-04
 20 <160> NUMBER OF SEQ ID NOS: 33
 22 <170> SOFTWARE: PatentIn/WordPerfect
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1843
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (3)...(1715)
 32 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from brain tissue
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 40 gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa        95
 41 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
 42                 20                  25                   30
 44 gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg       143
 45 Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
 46             35                  40                  45
 48 aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa       191
 49 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
 50         50                  55                  60
 52 gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct       239
 53 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala
 54         65                  70                  75
 56 cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat       287
 57 Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
 58  80                  85                  90                  95
 60 tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc       335
 61 Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu
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62                   100                  105                  110
64 cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat       383
65 Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp
66           115                  120                  125
68 gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa       431
69 Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys
70           130                  135                  140
72 atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc       479
73 Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala
74        145                  150                  155
76 aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg       527
77 Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp
78 160                  165                  170                  175
80 gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta       575
81 Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu
82           180                  185                  190
84 cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa       623
85 Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys
86           195                  200                  205
88 gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt       671
89 Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu
90           210                  215                  220
92 cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa       719
93 Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu
94        225                  230                  235
96 gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg       767
97 Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly
98 240                  245                  250                  255
100 aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag      815
101 Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys
102           260                  265                  270
104 att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa      863
105 Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu
106           275                  280                  285
108 gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt      911
109 Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg
110           290                  295                  300
112 act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa      959
113 Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln
114        305                  310                  315
116 tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa     1007
117 Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys
118 320                  325                  330                  335
120 aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac     1055
121 Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn
122           340                  345                  350
124 cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa     1103
125 Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys
126        355                  360                  365
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129 Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp
130         370             375             380
132 tat acc atg acc ttg ctg gat ttg ttt gaa gtg gag aag gat ggt gag       1199
133 Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu
134         385             390             395
136 aaa gaa gcc ttc aga gag gac ctt cat aac agg atg ctt cta tgg cat       1247
137 Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His
138 400             405             410             415
140 ggt tcc agg atg agt aac tgg gtg gga atc ttg agc cat ggg ctt cga       1295
141 Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg
142             420             425             430
144 att gcc cca cct gaa gct ccc atc aca ggt tac atg ttt ggg aaa gga       1343
145 Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly
146             435             440             445
148 atc tac ttt gct gac atg tct tcc aag agt gcc aat tac tgc ttt gcc       1391
149 Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala
150         450             455             460
152 tct cgc cta aag aat aca gga ctg ctg ctc tta tca gag gta gct cta       1439
153 Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu
154         465             470             475
156 ggt cag tgt aat gaa cta cta gag gcc aat cct aag gcc gaa gga ttg       1487
157 Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu
158 480             485             490             495
160 ctt caa ggt aaa cat agc acc aag ggg ctg ggc aag atg gct ccc agt       1535
161 Leu Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser
162             500             505             510
164 tct gcc cac ttc gtc acc ctg aat ggg agt aca gtg cca tta gga cca       1583
165 Ser Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro
166             515             520             525
168 gca agt gac aca gga att ctg aat cca gat ggt tat acc ctc aac tac       1631
169 Ala Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr
170         530             535             540
172 aat gaa tat att gta tat aac ccc aac cag gtc cgt atg cgg tac ctt       1679
173 Asn Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu
174         545             550             555
176 tta aag gtt cag ttt aat ttc ctt cag ctg tgg tga atgttgatat           1725
177 Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
178 560             565             570
180 taaataaacc agagatctga tcttcaagca agaaataag cagtgttgta cttgtgaatt      1785
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186 <211> LENGTH: 570
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 2
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198 Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys
199             35                  40                  45
201 Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp
202         50                  55                  60
204 Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala Pro
205 65                  70                  75                  80
207 Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys
208                 85                  90                  95
210 Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln
211             100                 105                 110
213 Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala
214         115                 120                 125
216 Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met
217     130                 135                 140
219 Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys
220 145                 150                 155                 160
222 Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu
223             165                 170                 175
225 Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln
226         180                 185                 190
228 Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu
229         195                 200                 205
231 Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg
232     210                 215                 220
234 Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu
235 225                 230                 235                 240
237 Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys
238             245                 250                 255
240 Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile
241         260                 265                 270
243 Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala
244     275                 280                 285
246 Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr
247     290                 295                 300
249 Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu
250 305                 310                 315                 320
252 Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr
253             325                 330                 335
255 Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu
256         340                 345                 350
258 His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val
259     355                 360                 365
261 Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
262 370                 375                 380
264 Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys
265 385                 390                 395                 400
267 Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly
268             405                 410                 415
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PATENT APPLICATION:  US/09/701,586C     TIME: 15:44:32

Input Set : A:\701586sq
Output Set: N:\CRF4\11132002\I701586C.raw
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270 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
271             420             425             430
273 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
274         435             440             445
276 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
277     450             455             460
279 Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly
280 465             470             475             480
282 Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
283             485             490             495
285 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
286             500             505             510
288 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
289         515             520             525
291 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
292     530             535             540
294 Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
295 545             550             555             560
297 Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
298             565             570
301 <210> SEQ ID NO: 3
302 <211> LENGTH: 2265
303 <212> TYPE: DNA
304 <213> ORGANISM: Homo sapiens
306 <220> FEATURE:
307 <221> NAME/KEY: CDS
308 <222> LOCATION: (242)...(1843)
309 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from uterus tissue
311 <400> SEQUENCE: 3
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315 tagccgatgt ctaatccccc acacaagctc atccccggcc tctgggattg ttgggaattc   120
317 tctccctaat tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag   180
319 gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc ttttcttggc   240
321 c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag       286
322   Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu
323   1               5                  10                  15
325 aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc tcc    334
326 Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser
327             20                  25                  30
329 acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc cgc    382
330 Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg
331         35                  40                  45
333 gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg tat    430
334 Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr
335         50                  55                  60
337 gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac aac    478
338 Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn
339     65                  70                  75
341 aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc    526
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/13/2002
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Input Set : A:\701586sq
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:13; Xaa Pos. 33,41,42,43,48
Seq#:14; Xaa Pos. 1,2,3,4,5,6,7,9,10,11,12,13,14,16,17,18,19,20,21
Seq#:15; Xaa Pos. 2,3,4,5,6,7,8,9,10,12,13,15,16,20,21,22,23,24,25,26,27,28
Seq#:15; Xaa Pos. 29,30,31,32
Seq#:16; Xaa Pos. 2,3,4,6,8,9,10,11,14,16,18,19,20,21,22,24,25,26,28
Seq#:17; Xaa Pos. 2,4,5,6,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23,24,25
Seq#:17; Xaa Pos. 26,27,33,34,35,38,39,40,41,42,43
Seq#:18; Xaa Pos. 4,8,11,12,13
Seq#:19; Xaa Pos. 2,3,4,6,7,9,13,15,16
Seq#:20; Xaa Pos. 2,3,4,6
Seq#:21; Xaa Pos. 2,3,5,6,7,8,10,11,12,14,15,16,17,18,19,20,21,22,24,26,27
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